**Figure 1**

MRGPAVLLTV ALATLLAPGA GAPVQSQGSQ NKLLLVSEFDG FRWNYDQDVD
TPNLDAMARD GVKARYMTPA FVTMTSPCHF TLVTGKYIEN HGVVHNMYYN
TTSKVCLPYH ATLGQRWWD NGSVPIWITA QRQGLRAGSF FYPGGNVITYQ
GVAVTRSRKE GIAHNYKNET EWRANIDTVM AWFTEEDLDL VTLYFGEPDS
TGHRYGPESP ERREMVRQVD RTVGYLRESI ARNHLTDRLN LIITSDHGMT
TVDKRAGDLV EFHKFPNFTF RDIEFELLDY GPNGMLLPKE GRLEKVDAL
KDAHPKLHVV KKEAFPEAFH YANNPRVTPL LMYSDLGYVI HGRINVQFNN
GEHGFDNKDM DMKTIFRAVG PSFRAGLEVE PFESVHVYEL MCRLLGIVPE
ANDGHLATLL PMLHTESALP PDALLVADGP CLPSLSQAKG CMPLSPAAPT
PAWLLWCW

Figure 2

3/14

10 20 30 40 50 60 70
| | | | | | |
GTCCATCTGGAAGGCCAGCATGAGAGGCCCGCGTCCTCCTCACTGTGGCTCTGGCCACGCTCCTGGCTCCCGGGG
M R G P A V L L T V A L A T L L A P G A
80 90 100 110 120 130 140 150
| | | | | | |
CCGGAGCACCGGTACAAAGTCAGGGCTCCCAGAACAAGCTGCTCCTGGTGTCTTCGACGGCTTCCGCTGGAACCTACG
G A P V Q S Q G S Q N K L L L V S F D G F R W N Y D
160 170 180 190 200 210 220 230
| | | | | | |
ACCAGGACGTGGACACCCCAACCTGGACGCCATGGCCCGAGACGGGGTGAAGGCACGCTACATGACCCCGCCTTTG
Q D V D T P N L D A M A R D G V K A R Y M T P A F V
240 250 260 270 280 290 300 310
| | | | | | |
TCACCATGACCAGCCCCTGCCACTTCACCCTGGTCACCGGCAAATATATCGAGAACCACGGGGTGGTTTCAACATGT
T M T S P C H F T L V T G K Y I E N H G V V H N M Y
320 330 340 350 360 370 380 390
| | | | | | |
ACTACAACACCACCAGCAAGGTGAAGCTGCCCTACCACGCCACGCTGGGCATCCAGAGGTGGTGGGACAACGGCAGCG
Y N T T S K V K L P Y H A T L G I Q R W W D N G S V
400 410 420 430 440 450 460
| | | | | | |
TGCCCATCTGGATCACAGCCCAGAGGCAGGGCCTGAGGGCTGGCTCCTTCTTCTACCCGGGCGGGAACGTCACCTACC
P I W I T A Q R Q G L R A G S F F Y P G G N V T Y Q
470 480 490 500 510 520 530 540
| | | | | | |
AAGGGGTGGCTGTGACGCGGAGCCGGAAGAAGGCATCGCACACAACCTACAAAAATGAGACGGAGTGGAGAGCGAACA
G V A V T R S R K E G I A H N Y K N E T E W R A N I
550 560 570 580 590 600 610 620
| | | | | | |
TCGACACAGTGATGGCGTGGTTCACAGAGGAGGACCTGGATCTGGTCACACTCTACTTCGGGGAGCCGGACTCCACGG
D T V M A W F T E E D L D L V T L Y F G E P D S T G
630 640 650 660 670 680 690 700
| | | | | | |
GCCACAGGTACGGCCCCGAGTCCCCGAGAGGAGGGAGATGGTGCGGCAGGTGGACCGGACCGTGGGCTACCTCCGGG
H R Y G P E S P E R R E M V R Q V D R T V G Y L R E
710 720 730 740 750 760 770 780
| | | | | | |
AGAGCATCGCGCAACCACCTCACAGACCGCCTCAACCTGATCATCATCCGACCACGGCATGACGACCGTGGACA
S I A R N H L T D R L N L I I T S D H G M T T V D K

Figure 3a

790 800 810 820 830 840 850
AACGGGCTGGCGACCTGGTTGAATTCCACAAGTTCCCCAACTTCACCTTCGGGACATCGAGTTTGAGCTCCTGGACT
R A G D L V E F H K F P N F T F R D I E F E L L D Y

860 870 880 890 900 910 920 930
ACGGACCAAACGGGATGCTGCTCCCTAAAGAAGGGAGGCTGGAGAAGGTGTACGATGCCCTCAAGGACGCCACCCCA
G P N G M L L P K E G R L E K V Y D A L K D A H P K

940 950 960 970 980 990 1000 1010
AGCTCCACGTCTACAAGAAGGAGGCGTTCCCCGAGGCCTTCCACTACGCCAACAACCCCAGGGTCACACCCCTGCTGA
L H V Y K K E A F P E A F H Y A N N P R V T P L L M

1020 1030 1040 1050 1060 1070 1080 1090
TGTCACGCGACCTTGGCTACGTCATCCATGGGAGAATTAACGTCCAGTTCAACAATGGGGAGCACGGCTTTGACAACA
Y S D L G Y V I H G R I N V Q F N N G E H G F D N K

1100 1110 1120 1130 1140 1150 1160 1170
AGGACATGGACATGAAGACCATCTTCCGCGCTGTGGGCCCTAGCTTCAGGGCGGGCCTGGAGGTGGAGCCCTTTGAGA
D M D M K T I F R A V G P S F R A G L E V E P F E S

1180 1190 1200 1210 1220 1230 1240
GCGTCCACGTGTACGAGCTCATGTGCCGGCTGCTGGGCATCGTGCCCGAGGCCAACGATGGGCACCTAGCTACTCTGC
V H V Y E L M C R L L G I V P E A N D G H L A T L L

1250 1260 1270 1280 1290 1300 1310 1320
TGCCCATGCTGCACACAGAATCTGCTCTCCGCCTGATGCTCTGCTGGTCGCGGACGGACCCTGCCTCCCCAGCTTAT
P M L H T E S A L P P D A L L V A D G P C L P S L S

1330 1340 1350 1360 1370 1380 1390 1400
CCCAGGCCAGAGGCTGCATGCCACTGTCCCCGGCAGCGCCAACCCCTGCTTGGCTGTTATGGTGCTGGTAATAAGCCT
Q A R G C M P L S P A A P T P A W L L W C W

1410 1420 1430 1440 1450 1460 1470 1480
GCAGCCCAGGTCCAAAGCCCCGGCGAGCCGGTCCCATAAACGGCCCCCTGCCCTGCCCTGCTCCTGCTCCTCCCC
TTCGGGCCCCCTCCTCCTGCAAAACCCGCTCCCGAAGCGGCGCTGCCGTCTGCAGCCACGCGGGGGCGCGGGGAGTC

1490 1500 1510 1520 1530 1540 1550 1560
TTCTGCGGGCGCTGGAACCTGCAGACCCGGCCTCGGTACGCTGGGAGGGGCCCCGCCCGGCACAAAGCACCCATGGGA
TTCTGCGGGCGCTGGAACCTGCAGACCCGGCCTCGGTACGCTGGGAGGGGCCCCGCCCGGCACAAAGCACCCATGGGA

1640 1650 1660 1670 1680 1690 1700
ATAAAGGCCAAGCCGCGACAGTCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 3b

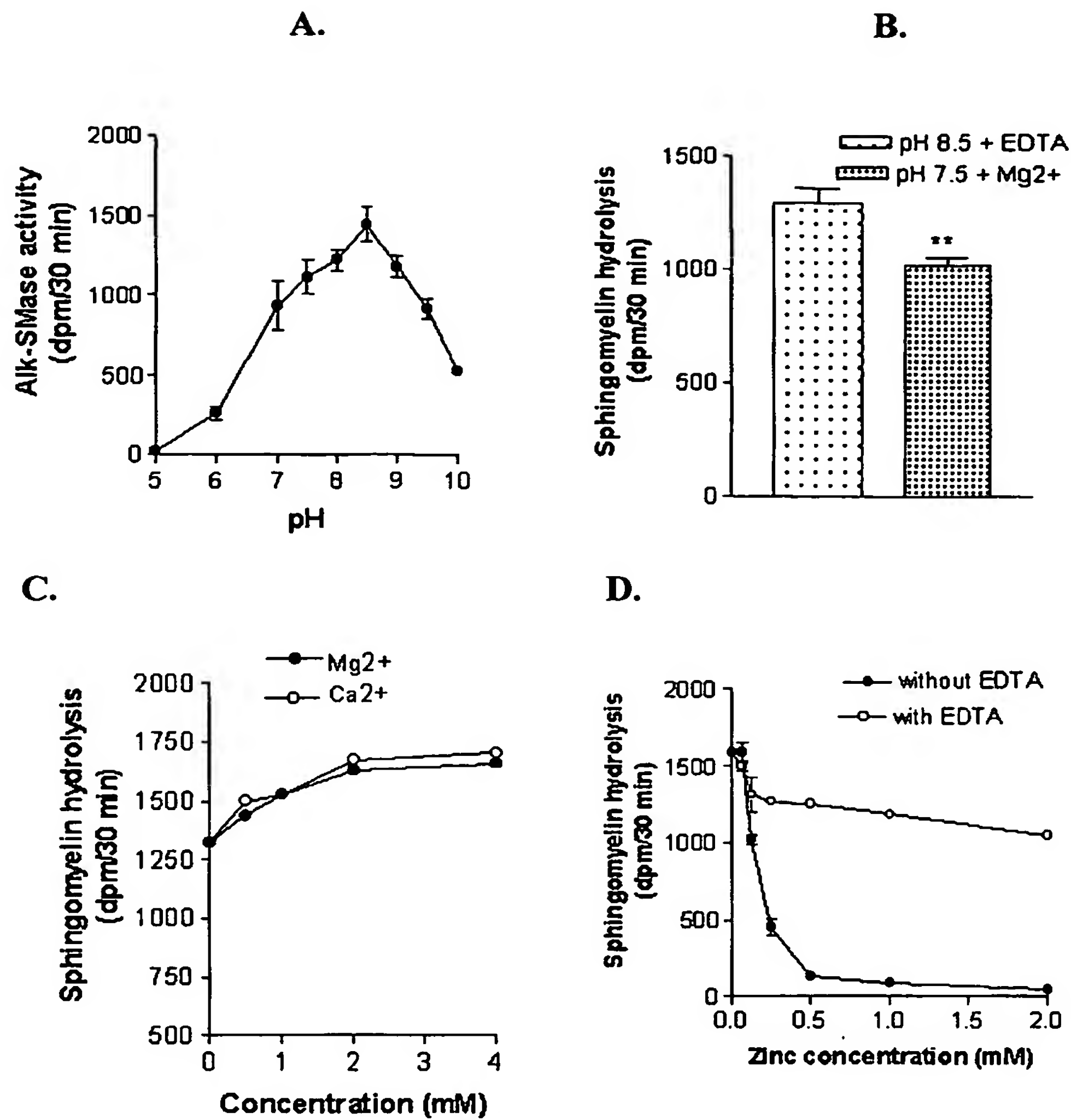
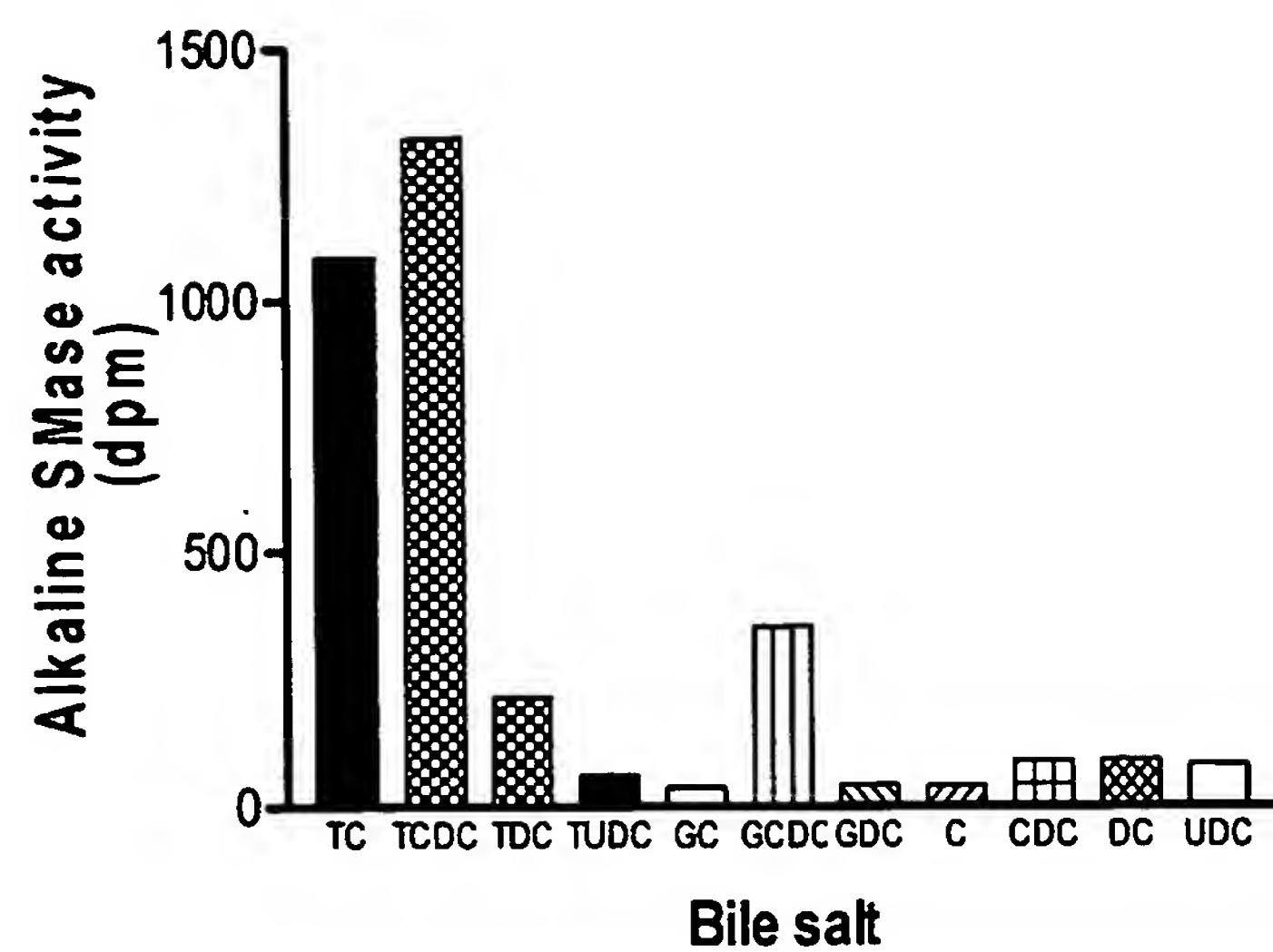
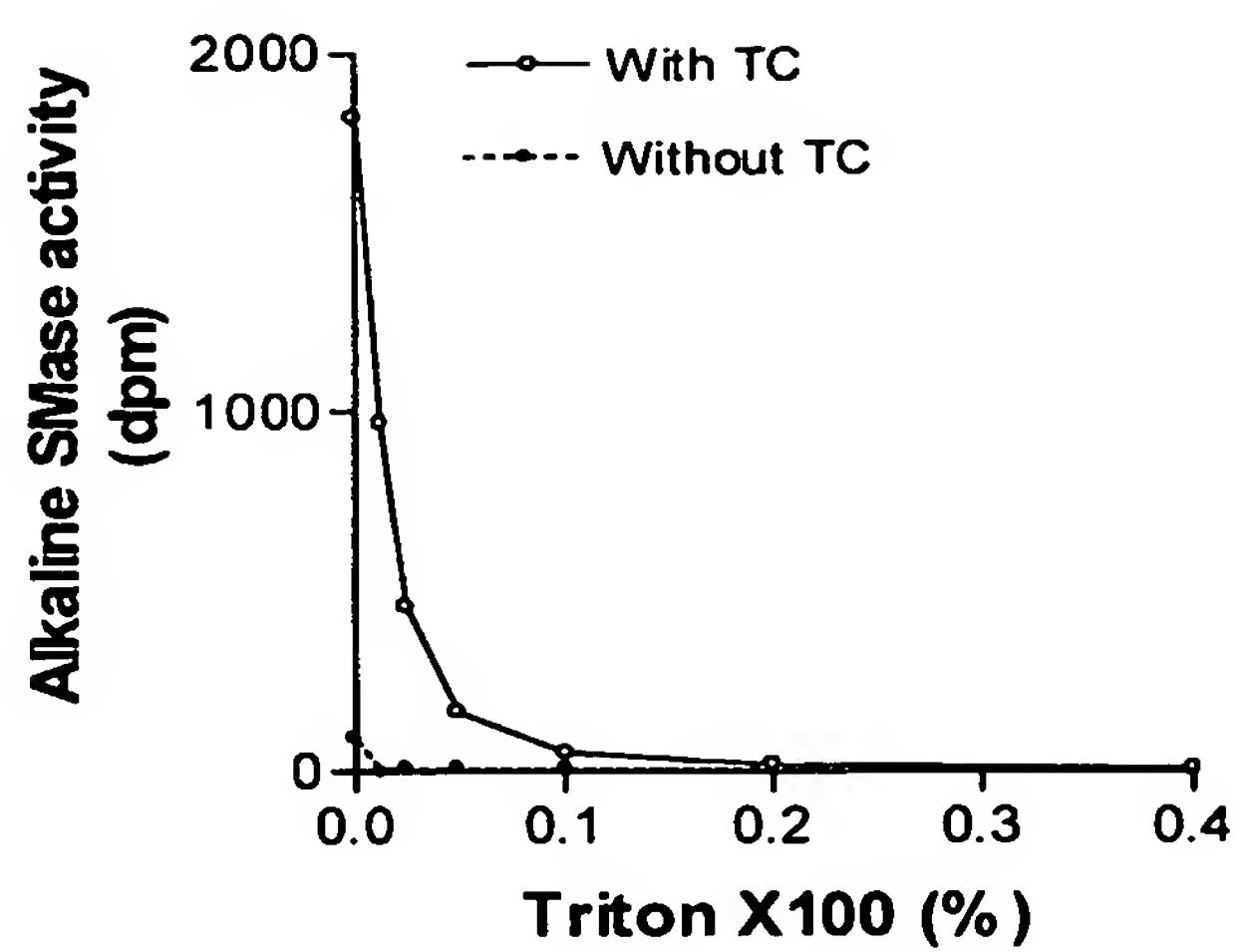


Figure 4

**Figure 5**

**Figure 6**

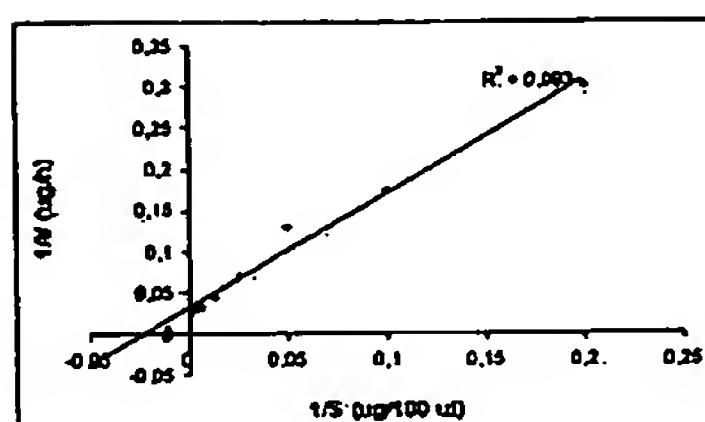
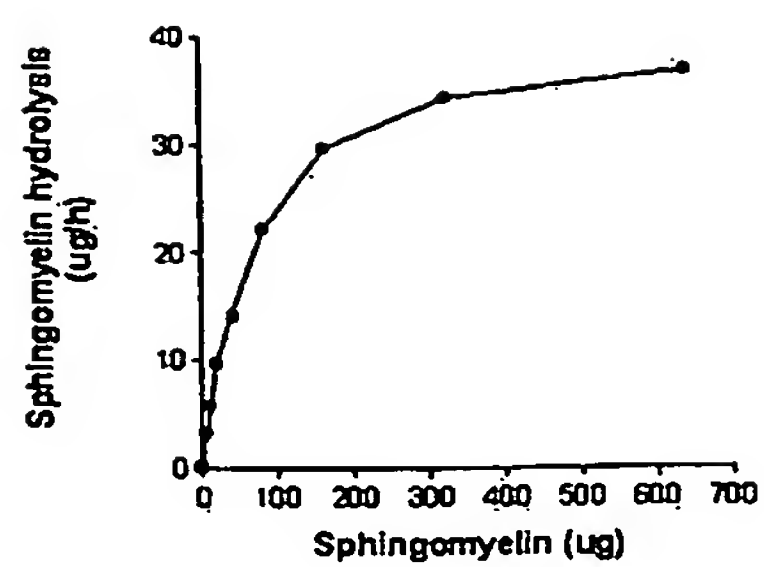


Figure 7

CTATTTAGGT GACACTATAG AACAAAGTTTG TACAAAAAAG CAGGCTGGTA
CCGGTCCGGA ATTCCCGGGA TGTCCATCTG GAAGGCCAG CATGAGAGGC
CCGGCCGTCC TCCTCACTGT GGCTCTGGCC ACGCTCCTGG CTCCCGGGGC
CGGAGCACCG GTACAAAGTC AGGGCTCCCA GAACAAGCTG CTCCTGGTGT
CCTTCGACGG CTTCCGCTGG AACTACGACC AGGACGTGGA CACCCCCAAC
CTGGACGCCA TGGCCCGAGA CGGGGTGAAG GCACGCTACA TGACCCCCGC
CTTTGTCACC ATGACCAGCC CCTGCCACTT CACCCTGGTC ACCGGCAAAT
ATATCGAGAA CCACGGGGTG GTTCACAACA TGTACTACAA CACCACCAGC
AAGGTGAAGC TGCCCTACCA CGCCACGCTG GGCATCCAGA GGTGGTGGGA
CAACGGCAGC GTGCCCATCT GGATCACAGC CCAGAGGCAG GGCCTGAGGG
CTGGCTCCTT CTTCTACCCG GCGGGGAACG TCACCTACCA AGGGGTGGCT
GTGACGCGGA GCCGGAAAGA AGGCATCGCA CACAACCTACA AAAATGAGAC
GGAGTGGAGA GCGAACATCG ACACAGTGAT GGCGTGGTTC ACAGAGGAGG
ACCTGGATCT GGTCACACTC TACTTCGGGG AGCCGGACTC CACGGGCCAC
AGGTACGGCC CCGAGTCCCC GGAGAGGAGG GAGATGGTGC GGCAGGTGGA
CCGGACCGTG GGCTACCTCC GGGAGAGCAT CGCGCGCAAC CACCTCACAG
ACCGCCTCAA CCTGATCATC ACATCCGACC ACGGCATGAC GACCGTGGAC
AAACGGGCTG GCGACCTGGT TGAATTCCAC AAGTTCCCCA ACTTCACCTT
CCGGGACATC GAGTTTGAGC TCCTGGACTA CGGACCAAAC GGGATGCTGC
TCCCTAAAGA AGGGAGGCTG GAGAAGGTGT ACGATGCCCT CAAGGACGCC
CACCCAAGC TCCACGTCTA CAAGAAGGAG GCGTTCCCCG AGGCCTTCCA
CTACGCCAAC AACCCAGGG TCACACCCCT GCTGATGTAC AGCGACCTTG
GCTACGTCAT CCATGGGAGA ATTAACGTCC AGTTCAACAA TGGGGAGCAC
GGCTTTGACA ACAAGGACAT GGACATGAAG ACCATCTTCC GCGCTGTGGG
CCCTAGCTTC AGGGCGGGCC TGGAGGTGGA GCCCTTTGAG AGCGTCCACG
TGTACGAGCT CATGTGCCGG CTGCTGGGCA TCGTGCCCGA GGCCAACGAT
GGGCACCTAG CTACTCTGCT GCCCATGCTG CACACAGAAT CTGCTCTTCC
GCCTGATGCT CTGCTGGTGC CGGACGGACC CTGCCTCCCC AGCTTATCCC
AGGCCAAAGG CTGCATGCCA CTGTCCCCGG CAGCGCCAAC CCCTGCTTGG
CTGTTATGGT GCTGGTAATA AGCCTGCAGC CCAGGTCCAA AGCCCCCGGC
GAGCCGGTCC CATAACCGGC CCCCTGCCCC TGCCCCTGCT CCTGCTCCTC
CCCTTCGGGC CCCCTCCTCC TGCAAAACCC GCTCCCGAAG CGGCGCTGCC
GTCTGCAGCC ACGCGGGGGC GCGCGGGAGT CTTCTGCGGG CGCTGGAACC
TGCAGACCCG GCCTCGGTCA GCTGGGAGGG GCCCGCCCCG GCACAAAGCA
CCCATGGGAA TAAAGGCCAA GCCGCGACAG TCAGCAAAAA AAAAAAAAAA
AAAAAAAAAA AAAAAAAAAA AGGGCGGCCG CTCTAGAGTA TCCCTCGAGG
GGCCAAGCT TACGCGTACC CAGCTTTCTT GTACAAAGTG GTCCCTATAG
TGAGTCGTAT TATAAGCTAG GCA

Figure 8

10/14

Alk-SMase
NPP1_HUMAN -----MRGPAVLLTVALATLLAPGAGAPVQSQSQNKLLLVSEFGFRWNYDQD--VDT 51
NPP2_HUMAN KGDCCTNYQVVCKGESHVDDDCCEEIKAAECFAGFVRPPLIIFSVDFGFRASYMKKGSKVM 232
NPP3_HUMAN RGDCCTNYQVVCKGESHVDDDCCEEIKAAECFAGFVRPPLIIFSVDFGFRASYMKKGSKVM 186
NPP4_HUMAN KKDCCADYKSVCOGETSWLEENCOTAAQSQSQCEGFDLPPVILFSDGFRAEYLYTWDTLM 181
NPP5_HUMAN -----MKLLVILLFSGITGFRSDSSSSSLPP-----KLLLVSEFGFRADYLYK--YEF 46
-----MTSKFLLVSFILAALSSTTFSLOPD---QQKVLLVSEFGFRWDYLYK--VPT 48
* * * * *

Alk-SMase
NPP1_HUMAN PNLDAMARDGVKARYMTAFVTMTSPCHFTLVTKGYIENHGUVHNMYYNTTSKVLPYHA 111
NPP2_HUMAN PVISKLLKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGII DNKMYDPKMNASFSLKS 292
NPP3_HUMAN PNIEKLRSCGTHSPYMRPVYPTKTFPNLYTLATGLYPESHGII DNKMYDPKMNASFSLKS 246
NPP4_HUMAN PNINKLKTGCIHSGYMRAMYPTKTFPNHYSIVTGLYPESHGII DNKMYDPKMNASFSLKS 241
NPP5_HUMAN PHLQNFIEGVLVEHVKNVFTKTFPNHYSIVTGLYEEHSGIVANSMDAVTKKHFS--D 104
PHFHYIMKYGVHVQVTVNFTKTFPNHYSIVTGLYEEHSGIVANSMDAVTKKHFS--D 108
* * * * *

Alk-SMase
NPP1_HUMAN TLGIQRWWDNGSVPIWITAQR-QGLRAGSFFYPGGNVTYQGVAVTRSRKEGIAHNYKNET 170
NPP2_HUMAN KEKFNPEWYKGE-PIWVTAKY-QGLKSGTFFWPGSDVEINGIFPDIYKMYNGSVPFEEER- 349
NPP3_HUMAN REKFNHRWWGGQ-PLWITATK-QGVKAGTFFWS-----VVI PHERR- 285
NPP4_HUMAN KEQNNPAWWHGQ-PMWLTAMY-QGLKAATYFWPGSEVAINGSFPSIYMPYNGSVPFEEER- 298
NPP5_HUMAN SNDKDPFWWNEAVPIWITNQLQENRSSAAAMWPGTDVPIHDTISSYFMNYNSSVSFEER- 163
MNIYDSKFWEATPIWITNQR-AGHTSGAAMWPGTDVKIKRFPHTHYMPYNESVSFEER- 166
* * *

Alk-SMase
NPP1_HUMAN EWRANIDTVMAWTEEDLDLVTLYFGEPSTGFRYGP-ESPERREMVRQVDRTVGYLRES 229
NPP2_HUMAN --ILAVLQWLQPKDERPHFYTLYLEEPSSSGSYGP-VSSEVIKALQVRDGMVGMMLMDG 406
NPP3_HUMAN --ILTILQWLTLDPHERPSVYAFYSEQPFSGHRYGP-FGPMTNPLREIDKIVGQMLMDG 342
NPP4_HUMAN --ISTLLKWLDLPAERPRFYTMFEEDSSSGHAGGP-VSARVIKALQVVDHAFGMLMEG 355
NPP5_HUMAN --LNNITMWLNN-SNPPVTFATLYWEEPDASGHRKYGPEDKENMSRVLKKIDDLIGDLVQR 220
--VAKIIEWFT--SKEPINLGLLYWEDPDMDGHLGP-DSPLMGPVISDIDKKLGYLIQM 221
* * * * *

Alk-SMase
NPP1_HUMAN IARNHLDTRLNLIITSDEHGMTTVDKRAGDLVEFHKFPNFTFRDIEFELLDYGPNGMLLP- 288
NPP2_HUMAN LKELNLHRCNLNLIITSDEHGMEOGSCKK-----YIYLNKYLGDVKNIKVIYGPAAARLPS 460
NPP3_HUMAN LKQKLHRCNVNIFVGDHGMEDVTCR-----TEFLSNYLTNVDDITLVPGTLGRIR-- 394
NPP4_HUMAN LKQRLHNCVNIILLADHGMDOYTCNK-----MEYMTDYFPRINFFYMEGPAPRIRAH 409
NPP5_HUMAN LKMLGLWENLNVIIITSDEHGMTQCSQDR-----LINLDSCIDHSYTLIDLSPVAAILP- 273
LKKAKLWNTLNLIITSDEHGMTQCSQDR-----LIELDQYLDKDHYTLDLQSPVAAILP- 274
* * * * *

Alk-SMase
NPP1_HUMAN -----KEGRLEKVDALKDAHP--KLHVYKKEAFPEAFHYANNPRVTPLLMYSDLGVI 340
NPP2_HUMAN DVDPKYYSFNYEGIARNLSCREPNQHFYPYKHLKHLKRLHFAKSDRIEPLTFYLDPOWQL 520
NPP3_HUMAN SKFSNNAKYDFKAI IANLTCKKPDQHFYPYKHLKHLKRLHFAKSDRIEPLTFYLDPOWQL 454
NPP4_HUMAN NIPHDFFSFENSEI VRNLSCRKPDQHFYPYKHLKHLKRLHFAKSDRIEPLTFYLDPOWQL 469
NPP5_HUMAN -----KINR-TEVYNKLNKNSP--HMNVYKEDI PNRFYQHNDRIQPIILVADEGWTI 324
-----KEGKFDEVYEALTHAHP--NLTVYKKEDVPERWHYKYNRIQPII AVADEGWHI 326
* * * * *

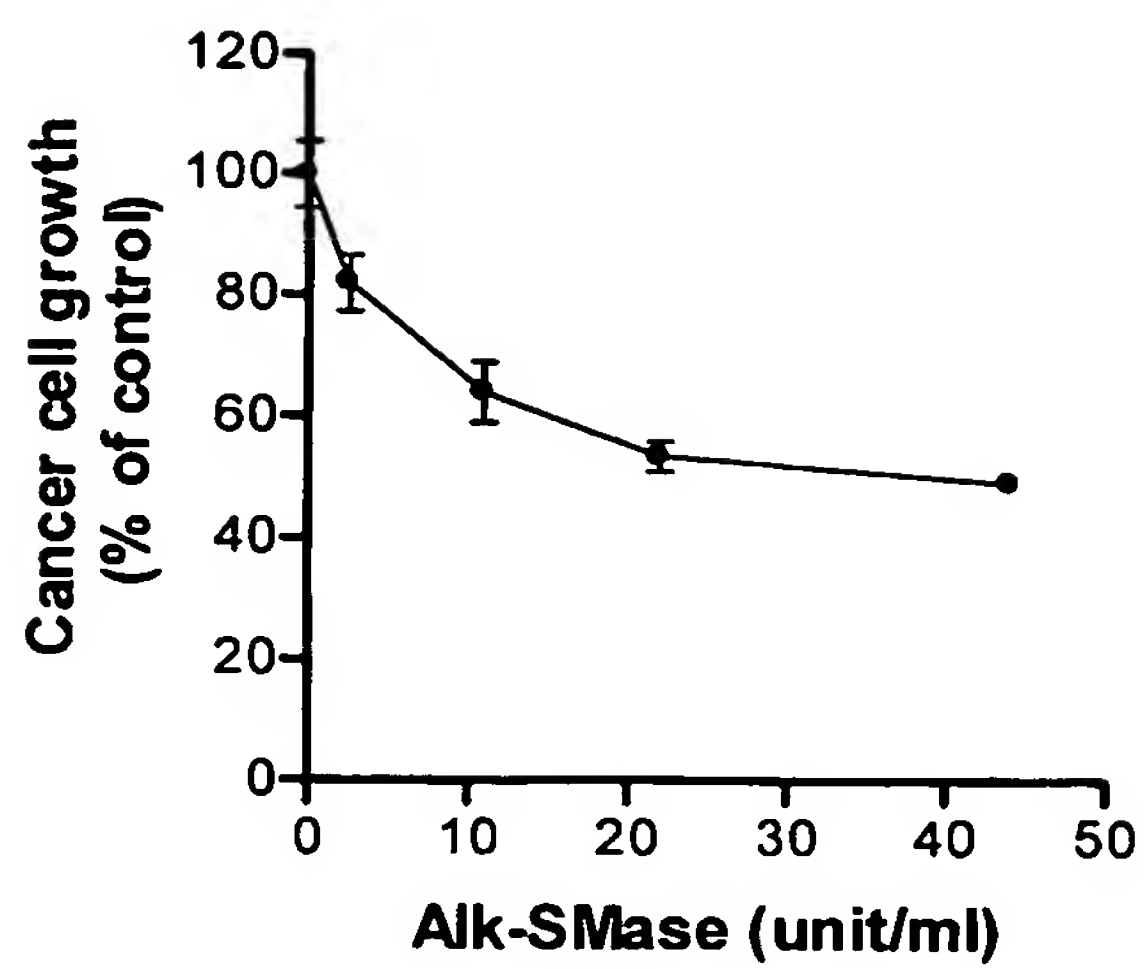
Alk-SMase
NPP1_HUMAN HGR-----INVQFNNGEFGDNKMDMKTIFRAVGPSFRAGLEVPEPFESVHVYELMC 392
NPP2_HUMAN ALN-----PSERKYCGSGFGSDNVFSNMQALFVGYPGFKHGIEADTFENIEVYNLMC 574
NPP3_HUMAN ARKPLDVYKKPSGKCFQGDHGFNDKVNMQTFVVGYPGFKHGIEADTFENIEVYNLMC 514
NPP4_HUMAN VRS-----KSN-TNCGGNHGYNNEFRSMEAI FLAHGPSFKEKTEVEPFENIEVYNLMC 522
NPP5_HUMAN VLN-----ESS-QKLGDNHGYDNLSPSMHPFLAAGHAPAFHKGKYSTINIVDIYPMCM 375
LQN-----KSDDFLLGNHGYDNALADMHPIFLAAGHAPAFRKNFSKEAMNSTDLYPLLC 378
* * * * *

Alk-SMase
NPP1_HUMAN RLLGIVPEANDGHLATLLPMLHT----- 415
NPP2_HUMAN DLLNLTAPANNNGTHGSLNHLLKNPVYTPKHPKEVHPLVQCPFTR-NPRDNLGCSCN--PS 631
NPP3_HUMAN DLLGLKPAPANNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMYLQSDFDLGCTCD---D 571
NPP4_HUMAN DLLRIQAPANNNGTHGSLNHLLKVPFYEPASHAEVSKFSVCGFANPLPTESLDCFCPLQN 582
NPP5_HUMAN HILGLKPHPNNGTFGHTKCLL-----VDQWCINLP----- 405
HLLNITAMPHNGSFWNVQDLNLSAMPRVVPYTQSTILLPG----- 418
* * *

Alk-SMase
NPP1_HUMAN -----ESALPPDALLVADGPC 431
NPP2_HUMAN ILPIEDFQTQFNLTVAEEKI IKHETLPYGRPRVLQKENTICLLSQHQFMSGYSQDILMPL 691
NPP3_HUMAN KVEPKNKLDELNKLRLHTKGSTEERHLLYGRPAVLYR-TRYDILYHTDFESGYSEIFLMPL 630
NPP4_HUMAN STQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREYVSGFGKAMRMPM 642
NPP5_HUMAN -----EAI AIVIGSLLVLTMLTCLIIIM 428
-----SVKPAEYDQEGSYPYFIGVSLGSIIVIVFFVIF 451

Alk-SMase
NPP1_HUMAN LPSLSQAKGCMPLSPAAPTFAWLLWCW----- 458
NPP2_HUMAN WTSYTVDRNDSFS--TEDFSNCYQDFRIPLSPVHKCSFYKNNTKVSYGFLSPQLNKNS 749
NPP3_HUMAN WTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPSFSQNCAYKNDKQMSYGFLEPPYLSSSP 690
NPP4_HUMAN WSSYTVPLQGDTSPLPPTVPDCLRADVRVPPSESQKCSFYLAADKNITHGFLYPPASNRTS 702
NPP5_HUMAN QNRLSVPRPFSRLQLQEDDDDDPLIG----- 453
IKHLIHSQIPALQDMHAEIAQPLQA----- 477

Figure 9

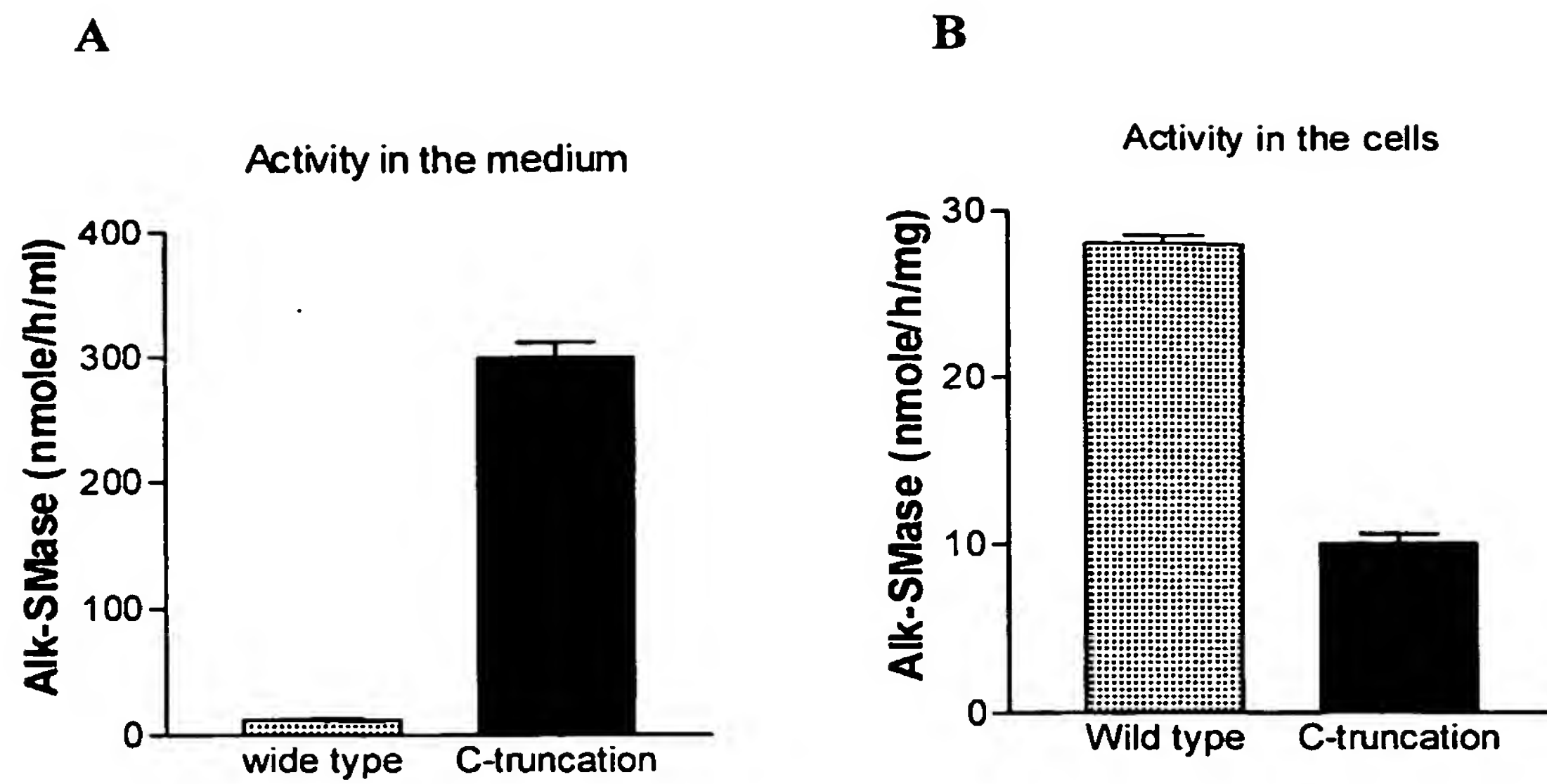
**Figure 10**

MRGPAVLLTV ALATLLAPGA GAPVQSQGSQ NKLLLVSF DG FRWNYDQDVD TPNLDAMARD 60
GVKARYMTPA FVTMTSPCHF TLVTGKYIEN HGVVHNMYYN TTSKV KLPYH ATLG IQRWWD 120
NGSVPIWITA QRQGLRAGSF FYPGGNV TYQ GVAVTRSRKE GIAHNYKNET EWRANIDTVM 180
AWFTEEDLDL VTLYFGEPDS TGHRYGPESP ERREMVRQVD RTVGYLRESI ARNHLTDRLN 240
LIITSDHGMT TVDKRAGDLV EFHKFPNFTF RDIEFELLDY GPNGMLLPKE GRLEKVYDAL 300
KDAHPKLH VY KKEAFPEAFH YANNPRVTPL LMYSDLGYVI HGRINVQFNN GEHGFDNKDM 360
DMKTIFRAVG PSFRAGLEVE PFESVHVYEL MCRL LGIVPE ANDGHLATLL PMLHTESALP 420
PDGRPTLLPK GRSALPPSSR PLLVMG LLGT VILLSEVA 458

Figure 11

GTCCATCTGG	AAGGCCCAGC	ATGAGAGGCC	CGGCCGTCCT	CCTCACTGTG	50
GCTCTGGCCA	CGCTCCTGGC	TCCCGGGGCC	GGAGCACCGG	TACAAAGTCA	100
GGGCTCCCAG	AACAAGCTGC	TCCTGGTGTC	CTTCGACGGC	TTCCGCTGGA	150
ACTACGACCA	GGACGTGGAC	ACCCCCAACC	TGGACGCCAT	GGCCCGAGAC	200
GGGGTGAAGG	CACGCTACAT	GACCCCCGCC	TTTGTACCA	TGACCAGCCC	250
CTGCCACTTC	ACCCTGGTCA	CCGGCAAATA	TATCGAGAAC	CACGGGGTGG	300
TTCACAACAT	GTACTACAAC	ACCACCAGCA	AGGTGAAGCT	GCCCTACCAC	350
GCCACGCTGG	GCATCCAGAG	GTGGTGGGAC	AACGGCAGCG	TGCCCATCTG	400
GATCACAGCC	CAGAGGCAGG	GCCTGAGGGC	TGGCTCCTTC	TTCTACCCGG	450
GCGGGAACGT	CACCTACCAA	GGGGTGGCTG	TGACGCGGAG	CCGGAAAGAA	500
GGCATCGCAC	ACAATAACAA	AAATGAGACG	GAGTGGAGAG	CGAACATCGA	550
CACAGTGATG	GCGTGGTTCA	CAGAGGAGGA	CCTGGATCTG	GTCACACTCT	600
ACTTCGGGGA	GCCGGACTCC	ACGGGCCACA	GGTACGGCCC	CGAGTCCCCG	650
GAGAGGAGGG	AGATGGTGCG	GCAGGTGGAC	CGGACCGTGG	GCTACCTCCG	700
GGAGAGCATC	GCGCGCAACC	ACCTCACAGA	CCGCCTCAAC	CTGATCATCA	750
CATCCGACCA	CGGCATGACG	ACCGTGGACA	AACGGGCTGG	CGACCTGGTT	800
GAATTCCACA	AGTTCCCCAA	CTTCACCTTC	CGGGACATCG	AGTTTGAGCT	850
CCTGGACTAC	GGACCAAACG	GGATGCTGCT	CCCTAAAGAA	GGGAGGCTGG	900
AGAA _n GTGTA	CGATGCCCTC	AAGGACGCCC	ACCCCAAGCT	CCACGTCTAC	950
AAGAAGGAGG	CGTTCCCCGA	GGCCTTCCAC	TACGCCAACA	ACCCAGGGT	1000
CACACCCCTG	CTGATGTACA	GCGACCTTGG	CTACGTCATC	CATGGGAGAA	1050
TTAACGTCCA	GTTCAACAAT	GGGGAGCACG	GCTTTGACAA	CAAGGACATG	1100
GACATGAAGA	CCATCTTCCG	CGCTGTGGGC	CCTAGCTTCA	GGGCGGGCCT	1150
GGAGGTGGAG	CCCTTTGAGA	GCGTCCACGT	GTACGAGCTC	ATGTGCCGGC	1200
TGCTGGGCAT	CGTGCCCGAG	GCCAACGATG	GGCACCTAGC	TACTCTGCTG	1250
CCCATGCTGC	ACACAGAATC	TGCTCTTCCG	CCTGATGGAA	GGCCTACTCT	1300
CCTGCCCAAG	GGAAGATCTG	CTCTCCCGCC	CAGCAGCAGG	CCCCTCCTCG	1350
TGATGGGACT	GCTGGGGACC	GTGATTCTTC	TGTCTGAGGT	CGCATAACGC	1400
CCCATGGCTC	AAGGAAGCCG	CCGGGAGCTG	CCCGCAGGCC	CTGGGCGGCG	1450
TGTCTCGCTG	CGATGCTCTG	CTGGTCGCGG	ACGGACCCTG	CCTCCCCAGC	1500
TTATCCCAGG	CCAGAGGCTG	CATGCCACTG	TCCCGGGCAG	CGCCAACCCC	1550
TGCTTGGCTG	TTATGGTGCT	GGTAATAAGC	CTCGCAGCCC	AGGTCCAGAG	1600
CCCCCGGCGA	GCCGGTCCCA	TAACCGGCC	CCTGCCCCCTG	CCCCTGCTCC	1650
TGCTCCTCCC	CTTCGGGGCC	CCTCCTCCTG	CAAAACCCGC	TCCCGAAGCG	1700
GCGCTGCCGT	CTGCAGCCAC	GCGGGGGCGC	GCGGGAGCTC	TGCGGGCGCT	1750
GGAACCTGCA	GACCCGGCCT	CGGTCAGCTG	GGAGGGGCCC	GCCCCGGCAC	1800
AAAGCACCCA	TGGGAATAAA	GGCCAAGCCG	CGACAGTCAG	CAAAAAAAAA	1841
AAAAAAAAAAAAAAAAAAAAAAAAAAAA					

Figure 12

**Figure 13**